

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ryals, John
Friedrich, Leslie
Uknes, Scott
Molina, Antonio
Ruess, Wilhelm
Knauf-Beiter, Gertrude
Kung, Ruth
Kessmann, Helmut
Oostendorp, Michael

(ii) TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS

(iii) NUMBER OF SEQUENCES: 32

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Novartis Corporation
(B) STREET: 3054 Cornwallis Road
(C) CITY: Research Triangle Park
(D) STATE: North Carolina
(E) COUNTRY: USA
(F) ZIP: 27709

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/761,543
(B) FILING DATE: 6-DEC-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/034,378
(B) FILING DATE: 27-DEC-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/034,379
(B) FILING DATE: 27-DEC-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/034,382
(B) FILING DATE: 27-DEC-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/034,730
(B) FILING DATE: 10-JAN-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/035,021
(B) FILING DATE: 10-JAN-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/035,022

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(B) FILING DATE: 10-JAN-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/035,024

(B) FILING DATE: 10-JAN-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/875,015

(B) FILING DATE: 16-JUL-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Meigs, J. Timothy

(B) REGISTRATION NUMBER: 38,241

(C) REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (919) 541-8587

(B) TELEFAX: (919) 541-8689

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5655 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 2787..3347

(D) OTHER INFORMATION: /product= "1st exon of NIM1"

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 3427..4162

(D) OTHER INFORMATION: /product= "2nd exon of NIM1"

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 4271..4474

(D) OTHER INFORMATION: /product= "3rd exon of NIM1"

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 4586..4866

(D) OTHER INFORMATION: /product= "4th exon of NIM1"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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60

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TGGGATATGT	CATTGGGTTT	AGCGGTAATC	GGATTGAACC	CTTTCCGGTA	TAAAATACAA	180
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ACTTTTATGT	GCGAAGTTTT	CGATTCTGAT	TCGTTTACCT	GGAAGAGATT	AGAAAATTTG	300
CGTCTACCAA	AAACAGACAG	ATTAATTTTT	TCCAACCCGA	TACAAGTTTC	GGGGTTCTTG	360
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TTGATTACGT	GGACTCCAAG	CAACGACGTT	GTATTGTTTC	GTAGTAGTGA	TCGTGGTTGC	660
CTCTACAACA	TAAACGCAGA	GAAGTTGAAT	TTAGTTTATG	CAAAAAAAGA	GGGATCTGAT	720
TGTTCTTTTCG	TTTGTTTTCC	GTTTTGTTCT	GATTACGAGA	GGGTTGATCT	GAACGGAAGA	780
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GTTGACAAGG	ATCTCAAGTC	TCAAGTCTCA	ATTGGCTCGC	TCATTGTGGG	GCATAAATAT	900
ATCTAGTGAT	GTTTAATTGT	TTTTTATAAG	GTAAAAAGGA	ATATTGAATT	TTGTTTCTTA	960
GGTTTATGTA	ATAATACCAA	ACATTGTTTT	ATGAATATTT	AATCTGATTT	TTTGGCTAGT	1020
TATTTTATTA	TATCAAGGGT	TCCTGTTTAT	AGTTGAAAAC	AGTTACTGTA	TAGAAAATAG	1080
TGTCCCAATT	TTCTCTCTTA	AATAATATAT	TAGTTAATAA	AAGATATTTT	AATATATTAG	1140
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TTACATATAT	TTATAGCTTA	CCAATATAAC	CCGTATCTAT	GTTTTATAAG	CTTTTATACA	1260
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AAATTTATTA	AATATTTGGC	AATTGGGTGT	TTATCTAAAG	TTTATCACAA	TATTTATCAA	1380
CTATAATAGA	TGGTAGAAGA	TAAAAAAATT	ATATCAGATT	GATTCAATTA	AATTTTATAA	1440
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TTAAAATCAT	ACAAATCTTA	TCCTAATTTA	ACTTATCATT	TAAGAAATAC	AAAAGTAAAA	1620
AACGCGGAAA	GCAATAATTT	ATTTACCTTA	TTATAACTCC	TATATAAAGT	ACTCTGTTTA	1680
TTCAACATAA	TCTTACGTTG	TTGTATT CAT	AGGCATCTTT	AACCTATCTT	TTCATTTTCT	1740
GATCTCGATC	GTTTTCGATC	CAACAAAATG	AGTCTACCGG	TGAGGAACCA	AGAGGTGATT	1800
ATGCAGATT C	CTTCTTCTTC	TCAGTTTCCA	GCAACATCGA	GTCCGGAAAA	CACCAATCAA	1860
GTGAAGGATG	AGCCAAATTT	GTTTAGACGT	GTTATGAATT	TGCTTTTACG	TCGTAGTTAT	1920
TGAAAAAGCT	GATTTATCGC	ATGATTCAGA	ACGAGAAGTT	GAAGGCAAAT	AACTAAAGAA	1980

GTCTTTTATA TGTATACAAT AATTGTTTTT AAATCAAATC CTAATTAAAA AAATATATTC	2040
ATTATGACTT TCATGTTTTT AATGTAATTT ATTCCTATAT CTATAATGAT TTTGTTGTGA	2100
AGAGCGTTTT CATTTGCTAT AGAACAAGGA GAATAGTTCC AGGAAATATT CGACTTGATT	2160
TAATTATAGT GTAAACATGC TGAACACTGA AAATTACTTT TTCAATAAAC GAAAAATATA	2220
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ATATATTTAT ATCATCTCCA AATCTAGTTT GGTTTCAGGGG CTTACCGAAC CGGATTGAAC	2460
TTCTCATATA CAAAAATTAG CAACACAAAA TGTCTCCGGT ATAAATACTA ACATTTATAA	2520
CCCGAACCGG TTTAGCTTCC TGTATATCT TTTTAAAAA GATCTCTGAC AAAGATTCCCT	2580
TTCTTGAAAA TTTACCGGTT TTGGTGAAAT GTAAACCGTG GGACGAGGAT GCTTCTTCAT	2640
ATCTCACCAC CACTCTCGTT GACTTGACTT GGCTCTGCTC GTCAATGGTT ATCTTCGATC	2700
TTTAACCAAA TCCAGTTGAT AAGGTCTCTT CGTTGATTAG CAGAGATCTC TTTAATTTGT	2760
GAATTTCAAT TCATCGGAAC CTGTTG ATG GAC ACC ACC ATT GAT GGA TTC GCC	2813
Met Asp Thr Thr Ile Asp Gly Phe Ala	
1 5	
GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC GCT ACC GAT AAC ACC	2861
Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val Ala Thr Asp Asn Thr	
10 15 20 25	
GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA GTA CTC ACC GGA CCT	2909
Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln Val Leu Thr Gly Pro	
30 35 40	
GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC TTC GAA TCC GTC TTT	2957
Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser Phe Glu Ser Val Phe	
45 50 55	
GAC TCG CCG GAT GAT TTC TAC AGC GAC GCT AAG CTT GTT CTC TCC GAC	3005
Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys Leu Val Leu Ser Asp	
60 65 70	
GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG TCA GCG AGA AGC TCT	3053
Gly Arg Glu Val Ser Phe His Arg Cys Val Leu Ser Ala Arg Ser Ser	
75 80 85	
TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG GAG AAA GAC TCC AAC	3101
Phe Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys Glu Lys Asp Ser Asn	
90 95 100 105	
AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG ATT GCC AAG GAT TAC	3149
Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile Ala Lys Asp Tyr	
110 115 120	
GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG GCT TAT GTT TAC AGC	3197
Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala Tyr Val Tyr Ser	
125 130 135	
AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT GAA TGC GCA GAC GAG	3245
Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala Asp Glu	
140 145 150	

AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG GAT TTC ATG TTG GAG	3293
Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met Leu Glu	
155 160 165	
GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT GAA TTA ATT ACT CTC	3341
Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile Thr Leu	
170 175 180 185	
TAT CAG GTAAAAACACC ATCTGCATTA AGCTATGGTT ACACATTCAT GAATATGTTT	3397
Tyr Gln	
TTACTTGAGT ACTTGATTTT GTATTTTCAG AGG CAC TTA TTG GAC GTT GTA GAC	3450
Arg His Leu Leu Asp Val Val Asp	
190 195	
AAA GTT GTT ATA GAG GAC ACA TTG GTT ATA CTC AAG CTT GCT AAT ATA	3498
Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile	
200 205 210	
TGT GGT AAA GCT TGT ATG AAG CTA TTG GAT AGA TGT AAA GAG ATT ATT	3546
Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile	
215 220 225	
GTC AAG TCT AAT GTA GAT ATG GTT AGT CTT GAA AAG TCA TTG CCG GAA	3594
Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu	
230 235 240	
GAG CTT GTT AAA GAG ATA ATT GAT AGA CGT AAA GAG CTT GGT TTG GAG	3642
Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu	
245 250 255	
GTA CCT AAA GTA AAG AAA CAT GTC TCG AAT GTA CAT AAG GCA CTT GAC	3690
Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp	
260 265 270 275	
TCG GAT GAT ATT GAG TTA GTC AAG TTG CTT TTG AAA GAG GAT CAC ACC	3738
Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr	
280 285 290	
AAT CTA GAT GAT GCG TGT GCT CTT CAT TTC GCT GTT GCA TAT TGC AAT	3786
Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn	
295 300 305	
GTG AAG ACC GCA ACA GAT CTT TTA AAA CTT GAT CTT GCC GAT GTC AAC	3834
Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn	
310 315 320	
CAT AGG AAT CCG AGG GGA TAT ACG GTG CTT CAT GTT GCT GCG ATG CGG	3882
His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg	
325 330 335	
AAG GAG CCA CAA TTG ATA CTA TCT CTA TTG GAA AAA GGT GCA AGT GCA	3930
Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala	
340 345 350 355	
TCA GAA GCA ACT TTG GAA GGT AGA ACC GCA CTC ATG ATC GCA AAA CAA	3978
Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln	
360 365 370	
GCC ACT ATG GCG GTT GAA TGT AAT AAT ATC CCG GAG CAA TGC AAG CAT	4026
Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His	
375 380 385	

TCT CTC AAA GGC CGA CTA TGT GTA GAA ATA CTA GAG CAA GAA GAC AAA	4074
Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys	
390 395 400	
CGA GAA CAA ATT CCT AGA GAT GTT CCT CCC TCT TTT GCA GTG GCG GCC	4122
Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala	
405 410 415	
GAT GAA TTG AAG ATG ACG CTG CTC GAT CTT GAA AAT AGA G	4162
Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg	
420 425 430	
GTATCTATCA AGTCTTATTT CTTATATGTT TGAATTAAAT TTATGTCCTC TCTATTAGGA	4222
AACTGAGTGA ACTAATGATA ACTATTCCTTT GTGTCGTCCA CTGTTTAG TT GCA CTT	4278
Val Ala Leu	435
GCT CAA CGT CTT TTT CCA ACG GAA GCA CAA GCT GCA ATG GAG ATC GCC	4326
Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala	
440 445 450	
GAA ATG AAG GGA ACA TGT GAG TTC ATA GTG ACT AGC CTC GAG CCT GAC	4374
Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp	
455 460 465	
CGT CTC ACT GGT ACG AAG AGA ACA TCA CCG GGT GTA AAG ATA GCA CCT	4422
Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro	
470 475 480	
TTC AGA ATC CTA GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA	4470
Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys	
485 490 495	
ACC G GTATGGATTC TCACCCACTT CATCGGACTC CTTATCACAA AAAACAAAAC	4524
Thr	
500	
TAAATGATCT TTAACATGG TTTTGTTACT TGCTGTCTGA CCTTGTTTTT TTTATCATCA	4584
G TG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC	4629
Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu	
505 510 515	
GAC CAG ATT ATG AAC TGT GAG GAC TTG ACT CAA CTG GCT TGC GGA GAA	4677
Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu	
520 525 530	
GAC GAC ACT GCT GAG AAA CGA CTA CAA AAG AAG CAA AGG TAC ATG GAA	4725
Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu	
535 540 545	
ATA CAA GAG ACA CTA AAG AAG GCC TTT AGT GAG GAC AAT TTG GAA TTA	4773
Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn Leu Glu Leu	
550 555 560	
GGA AAT TCG TCC CTG ACA GAT TCG ACT TCT TCC ACA TCG AAA TCA ACC	4821
Gly Asn Ser Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser Lys Ser Thr	
565 570 575	
GGT GGA AAG AGG TCT AAC CGT AAA CTC TCT CAT CGT CGT CGG TGA	4866
Gly Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg Arg *	
580 585 590	
GA CTCTTGCC TCTTAGTGTA ATTTTGTCTG TACCATATAA TTCTGTTTTT ATGATGACTG	4926

TAAC TGTTTA	TGTCTATCGT	TGGCGTCATA	TAGTTTCGCT	CTTCGTTTTG	CATCCTGTGT	4986
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AAAAGAATAT	TCAAGTTCCC	TGAAC TTCTG	GCAACATTCA	TGTTATATGT	ATCTTCCTAA	5226
TTCTTCCTTT	AACCTTTTGT	AAC TCGAATT	ACACAGCAAG	TTAGTTTCAG	GTCTAGAGAT	5286
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ATTTGTGAAT	GACACAAGTT	AACAATCCTT	TGCACCATT	CTGGGTGCAT	ACATGGAAAC	5406
TTCTTCGATT	GAAACTTCCC	ACATGTGCAG	GTGCGTTCGC	TGTCACTGAT	AGACCAAGAG	5466
ACTGAAAGCT	TTCACAAATT	GCCCTCAAAT	CTTCTGTTTC	TATCGTCATG	ACTCCATATC	5526
TCCGACCACT	GGTCATGAGC	CAGAGCCCAC	TGATTTTGAG	GGAATTGGGC	TAACCATTTT	5586
CGAGCTTCTG	AGTCCTTCTT	TTTGATGTCC	TTTATGTAGG	AATCAAATTC	TTCCTTCTGA	5646
CTTGTGGAT						5655

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Thr	Thr	Ile	Asp	Gly	Phe	Ala	Asp	Ser	Tyr	Glu	Ile	Ser	Ser
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Thr	Ser	Phe	Val	Ala	Thr	Asp	Asn	Thr	Asp	Ser	Ser	Ile	Val	Tyr	Leu
			20					25					30		
Ala	Ala	Glu	Gln	Val	Leu	Thr	Gly	Pro	Asp	Val	Ser	Ala	Leu	Gln	Leu
		35					40					45			
Leu	Ser	Asn	Ser	Phe	Glu	Ser	Val	Phe	Asp	Ser	Pro	Asp	Asp	Phe	Tyr
	50					55					60				
Ser	Asp	Ala	Lys	Leu	Val	Leu	Ser	Asp	Gly	Arg	Glu	Val	Ser	Phe	His
	65				70				75					80	
Arg	Cys	Val	Leu	Ser	Ala	Arg	Ser	Ser	Phe	Phe	Lys	Ser	Ala	Leu	Ala
				85					90					95	
Ala	Ala	Lys	Lys	Glu	Lys	Asp	Ser	Asn	Asn	Thr	Ala	Ala	Val	Lys	Leu
			100					105					110		
Glu	Leu	Lys	Glu	Ile	Ala	Lys	Asp	Tyr	Glu	Val	Gly	Phe	Asp	Ser	Val
		115					120					125			
Val	Thr	Val	Leu	Ala	Tyr	Val	Tyr	Ser	Ser	Arg	Val	Arg	Pro	Pro	Pro
		130					135				140				

Lys	Gly	Val	Ser	Glu	Cys	Ala	Asp	Glu	Asn	Cys	Cys	His	Val	Ala	Cys	
145					150					155					160	
Arg	Pro	Ala	Val	Asp	Phe	Met	Leu	Glu	Val	Leu	Tyr	Leu	Ala	Phe	Ile	
				165					170					175		
Phe	Lys	Ile	Pro	Glu	Leu	Ile	Thr	Leu	Tyr	Gln	Arg	His	Leu	Leu	Asp	
			180					185					190			
Val	Val	Asp	Lys	Val	Val	Ile	Glu	Asp	Thr	Leu	Val	Ile	Leu	Lys	Leu	
		195					200					205				
Ala	Asn	Ile	Cys	Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu	Asp	Arg	Cys	Lys	
	210					215					220					
Glu	Ile	Ile	Val	Lys	Ser	Asn	Val	Asp	Met	Val	Ser	Leu	Glu	Lys	Ser	
225					230					235					240	
Leu	Pro	Glu	Glu	Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg	Arg	Lys	Glu	Leu	
				245					250					255		
Gly	Leu	Glu	Val	Pro	Lys	Val	Lys	Lys	His	Val	Ser	Asn	Val	His	Lys	
			260					265					270			
Ala	Leu	Asp	Ser	Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu	Leu	Leu	Lys	Glu	
		275					280					285				
Asp	His	Thr	Asn	Leu	Asp	Asp	Ala	Cys	Ala	Leu	His	Phe	Ala	Val	Ala	
	290					295					300					
Tyr	Cys	Asn	Val	Lys	Thr	Ala	Thr	Asp	Leu	Leu	Lys	Leu	Asp	Leu	Ala	
305					310					315					320	
Asp	Val	Asn	His	Arg	Asn	Pro	Arg	Gly	Tyr	Thr	Val	Leu	His	Val	Ala	
			325					330					335			
Ala	Met	Arg	Lys	Glu	Pro	Gln	Leu	Ile	Leu	Ser	Leu	Leu	Glu	Lys	Gly	
			340					345					350			
Ala	Ser	Ala	Ser	Glu	Ala	Thr	Leu	Glu	Gly	Arg	Thr	Ala	Leu	Met	Ile	
		355					360					365				
Ala	Lys	Gln	Ala	Thr	Met	Ala	Val	Glu	Cys	Asn	Asn	Ile	Pro	Glu	Gln	
	370					375					380					
Cys	Lys	His	Ser	Leu	Lys	Gly	Arg	Leu	Cys	Val	Glu	Ile	Leu	Glu	Gln	
385					390					395					400	
Glu	Asp	Lys	Arg	Glu	Gln	Ile	Pro	Arg	Asp	Val	Pro	Pro	Ser	Phe	Ala	
				405					410					415		
Val	Ala	Ala	Asp	Glu	Leu	Lys	Met	Thr	Leu	Leu	Asp	Leu	Glu	Asn	Arg	
			420					425					430			
Val	Ala	Leu	Ala	Gln	Arg	Leu	Phe	Pro	Thr	Glu	Ala	Gln	Ala	Ala	Met	
		435					440					445				
Glu	Ile	Ala	Glu	Met	Lys	Gly	Thr	Cys	Glu	Phe	Ile	Val	Thr	Ser	Leu	
	450					455					460					
Glu	Pro	Asp	Arg	Leu	Thr	Gly	Thr	Lys	Arg	Thr	Ser	Pro	Gly	Val	Lys	
465					470					475					480	
Ile	Ala	Pro	Phe	Arg	Ile	Leu	Glu	Glu	His	Gln	Ser	Arg	Leu	Lys	Ala	

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	485		490		495
Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser	500		505		510
Ala Val Leu Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala	515		520		525
Cys Gly Glu Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg	530		535		540
Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn	545		550		555
Leu Glu Leu Gly Asn Ser Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser	565		570		575
Lys Ser Thr Gly Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg	580		585		590

Arg *

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Phe	Gln	Pro	Ala	Gly	His	Gly	Gln	Asp	Trp	Ala	Met	Glu	Gly	Pro
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Arg	Asp	Gly	Leu	Lys	Lys	Glu	Arg	Leu	Val	Asp	Asp	Arg	His	Asp	Ser
			20					25					30		
Gly	Leu	Asp	Ser	Met	Lys	Asp	Glu	Glu	Tyr	Glu	Gln	Met	Val	Lys	Glu
		35					40					45			
Leu	Arg	Glu	Ile	Arg	Leu	Gln	Pro	Gln	Glu	Ala	Pro	Leu	Ala	Ala	Glu
		50				55					60				
Pro	Trp	Lys	Gln	Gln	Leu	Thr	Glu	Asp	Gly	Asp	Ser	Phe	Leu	His	Leu
65					70				75					80	
Ala	Ile	Ile	His	Glu	Glu	Lys	Pro	Leu	Thr	Met	Glu	Val	Ile	Gly	Gln
			85						90					95	
Val	Lys	Gly	Asp	Leu	Ala	Phe	Leu	Asn	Phe	Gln	Asn	Asn	Leu	Gln	Gln
			100					105					110		
Thr	Pro	Leu	His	Leu	Ala	Val	Ile	Thr	Asn	Gln	Pro	Gly	Ile	Ala	Glu
		115					120					125			
Ala	Leu	Leu	Lys	Ala	Gly	Cys	Asp	Pro	Glu	Leu	Arg	Asp	Phe	Arg	Gly
		130				135					140				

Asn Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser Val
145 150 155 160

Ala Val Leu Thr Gln Thr Cys Thr Pro Gln His Leu His Ser Val Leu
165 170 175

Gln Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser Thr
180 185 190

His Gly Tyr Leu Ala Ile Val Glu His Leu Val Thr Leu Gly Ala Asp
195 200 205

Val Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu Ala
210 215 220

Val Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Leu Lys Cys Gly
225 230 235 240

Ala Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu
245 250 255

Thr Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Gln Leu Gly Gln Leu
260 265 270

Thr Leu Glu Asn Leu Gln Met Leu Pro Glu Ser Glu Asp Glu Glu Ser
275 280 285

Tyr Asp Thr Glu Ser Glu Phe Thr Glu Asp Glu Leu Pro Tyr Asp Asp
290 295 300

Cys Val Phe Gly Gly Gln Arg Leu Thr Leu
305 310

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Gln Pro Ala Gly His Gly Gln Asp Trp Ala Met Glu Gly Pro
1 5 10 15

Arg Asp Gly Leu Lys Lys Glu Arg Leu Val Asp Asp Arg His Asp Ser
20 25 30

Gly Leu Asp Ser Met Lys Asp Glu Asp Tyr Glu Gln Met Val Lys Glu
35 40 45

Leu Arg Glu Ile Arg Leu Gln Pro Gln Glu Ala Pro Leu Ala Ala Glu
50 55 60

Pro Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His Leu
65 70 75 80

Ala	Ile	Ile	His	Glu	Glu	Lys	Thr	Leu	Thr	Met	Glu	Val	Ile	Gly	Gln	
				85					90					95		
Val	Lys	Gly	Asp	Leu	Ala	Phe	Leu	Asn	Phe	Gln	Asn	Asn	Leu	Gln	Gln	
			100					105					110			
Thr	Pro	Leu	His	Leu	Ala	Val	Ile	Thr	Asn	Gln	Pro	Gly	Ile	Ala	Glu	
		115					120					125				
Ala	Leu	Leu	Lys	Ala	Gly	Cys	Asp	Pro	Glu	Leu	Arg	Asp	Phe	Arg	Gly	
	130					135					140					
Asn	Thr	Pro	Leu	His	Leu	Ala	Cys	Glu	Gln	Gly	Cys	Leu	Ala	Ser	Val	
145					150					155					160	
Ala	Val	Leu	Thr	Gln	Thr	Cys	Thr	Pro	Gln	His	Leu	His	Ser	Val	Leu	
				165					170					175		
Gln	Ala	Thr	Asn	Tyr	Asn	Gly	His	Thr	Cys	Leu	His	Leu	Ala	Ser	Ile	
			180					185					190			
His	Gly	Tyr	Leu	Gly	Ile	Val	Glu	His	Leu	Val	Thr	Leu	Gly	Ala	Asp	
		195					200					205				
Val	Asn	Ala	Gln	Glu	Pro	Cys	Asn	Gly	Arg	Thr	Ala	Leu	His	Leu	Ala	
	210					215					220					
Val	Asp	Leu	Gln	Asn	Pro	Asp	Leu	Val	Ser	Leu	Leu	Leu	Lys	Cys	Gly	
225					230					235					240	
Ala	Asp	Val	Asn	Arg	Val	Thr	Tyr	Gln	Gly	Tyr	Ser	Pro	Tyr	Gln	Leu	
				245					250					255		
Thr	Trp	Gly	Arg	Pro	Ser	Thr	Arg	Ile	Gln	Gln	Gln	Leu	Gly	Gln	Leu	
			260					265					270			
Thr	Leu	Glu	Asn	Leu	Gln	Thr	Leu	Pro	Glu	Ser	Glu	Asp	Glu	Glu	Ser	
		275					280					285				
Tyr	Asp	Thr	Glu	Ser	Glu	Phe	Thr	Glu	Asp	Glu	Leu	Pro	Tyr	Asp	Asp	
	290					295					300					
Cys	Val	Phe	Gly	Gly	Gln	Arg	Leu	Thr	Leu							
305					310											

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Phe	Gln	Pro	Ala	Glu	Pro	Gly	Gln	Glu	Trp	Ala	Met	Glu	Gly	Pro	
1				5					10					15		
Arg	Asp	Ala	Leu	Lys	Lys	Glu	Arg	Leu	Leu	Asp	Asp	Arg	His	Asp	Ser	

20					25					30					
Gly	Leu	Asp	Ser	Met	Lys	Asp	Glu	Glu	Tyr	Glu	Gln	Met	Val	Lys	Glu
	35						40					45			
Leu	Arg	Glu	Ile	Arg	Leu	Glu	Pro	Gln	Glu	Ala	Pro	Arg	Gly	Ala	Glu
	50					55					60				
Pro	Trp	Lys	Gln	Gln	Leu	Thr	Glu	Asp	Gly	Asp	Ser	Phe	Leu	His	Leu
	65					70					75				80
Ala	Ile	Ile	His	Glu	Glu	Lys	Ala	Leu	Thr	Met	Glu	Val	Val	Arg	Gln
				85					90					95	
Val	Lys	Gly	Asp	Leu	Ala	Phe	Leu	Asn	Phe	Gln	Asn	Asn	Leu	Gln	Gln
			100					105					110		
Thr	Pro	Leu	His	Leu	Ala	Val	Ile	Thr	Asn	Gln	Pro	Glu	Ile	Ala	Glu
		115					120					125			
Ala	Leu	Leu	Glu	Ala	Gly	Cys	Asp	Pro	Glu	Leu	Arg	Asp	Phe	Arg	Gly
	130					135					140				
Asn	Thr	Pro	Leu	His	Leu	Ala	Cys	Glu	Gln	Gly	Cys	Leu	Ala	Ser	Val
	145					150					155				160
Gly	Val	Leu	Thr	Gln	Pro	Arg	Gly	Thr	Gln	His	Leu	His	Ser	Ile	Leu
				165					170					175	
Gln	Ala	Thr	Asn	Tyr	Asn	Gly	His	Thr	Cys	Leu	His	Leu	Ala	Ser	Ile
			180					185					190		
His	Gly	Tyr	Leu	Gly	Ile	Val	Glu	Leu	Leu	Val	Ser	Leu	Gly	Ala	Asp
		195					200					205			
Val	Asn	Ala	Gln	Glu	Pro	Cys	Asn	Gly	Arg	Thr	Ala	Leu	His	Leu	Ala
	210					215					220				
Val	Asp	Leu	Gln	Asn	Pro	Asp	Leu	Val	Ser	Leu	Leu	Leu	Lys	Cys	Gly
	225					230					235				240
Ala	Asp	Val	Asn	Arg	Val	Thr	Tyr	Gln	Gly	Tyr	Ser	Pro	Tyr	Gln	Leu
				245					250					255	
Thr	Trp	Gly	Arg	Pro	Ser	Thr	Arg	Ile	Gln	Gln	Gln	Leu	Gly	Gln	Leu
			260					265					270		
Thr	Leu	Glu	Asn	Leu	Gln	Met	Leu	Pro	Glu	Ser	Glu	Asp	Glu	Glu	Ser
		275					280					285			
Tyr	Asp	Thr	Glu	Ser	Glu	Phe	Thr	Glu	Asp	Glu	Leu	Pro	Tyr	Asp	Asp
	290					295					300				
Cys	Val	Leu	Gly	Gly	Gln	Arg	Leu	Thr	Leu						
	305					310									

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2011 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Arabidopsis thaliana

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..2011
 (D) OTHER INFORMATION: /note= "NIM1 cDNA sequence"

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 43..1824
 (D) OTHER INFORMATION: /product= "NIM1 protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCTCTTTA ATTTGTGAAT TTCAATTCAT CGGAACCTGT TG ATG GAC ACC ACC	54
Met Asp Thr Thr	
1	
ATT GAT GGA TTC GCC GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC	102
Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val	
5 10 15 20	
GCT ACC GAT AAC ACC GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA	150
Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln	
25 30 35	
GTA CTC ACC GGA CCT GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC	198
Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser	
40 45 50	
TTC GAA TCC GTC TTT GAC TCG CCG GAT GAT TTC TAC AGC GAC GCT AAG	246
Phe Glu Ser Val Phe Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys	
55 60 65	
CTT GTT CTC TCC GAC GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG	294
Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu	
70 75 80	
TCA GCG AGA AGC TCT TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG	342
Ser Ala Arg Ser Ser Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys	
85 90 95 100	
GAG AAA GAC TCC AAC AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG	390
Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu	
105 110 115	
ATT GCC AAG GAT TAC GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG	438
Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu	
120 125 130	
GCT TAT GTT TAC AGC AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT	486
Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser	
135 140 145	
GAA TGC GCA GAC GAG AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG	534
Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val	
150 155 160	
GAT TTC ATG TTG GAG GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT	582
Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro	
165 170 175 180	

10016236 121201

GAA	TTA	ATT	ACT	CTC	TAT	CAG	AGG	CAC	TTA	TTG	GAC	GTT	GTA	GAC	AAA	630
Glu	Leu	Ile	Thr	Leu	Tyr	Gln	Arg	His	Leu	Leu	Asp	Val	Val	Asp	Lys	
				185					190					195		
GTT	GTT	ATA	GAG	GAC	ACA	TTG	GTT	ATA	CTC	AAG	CTT	GCT	AAT	ATA	TGT	678
Val	Val	Ile	Glu	Asp	Thr	Leu	Val	Ile	Leu	Lys	Leu	Ala	Asn	Ile	Cys	
			200					205					210			
GGT	AAA	GCT	TGT	ATG	AAG	CTA	TTG	GAT	AGA	TGT	AAA	GAG	ATT	ATT	GTC	726
Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu	Asp	Arg	Cys	Lys	Glu	Ile	Ile	Val	
		215					220					225				
AAG	TCT	AAT	GTA	GAT	ATG	GTT	AGT	CTT	GAA	AAG	TCA	TTG	CCG	GAA	GAG	774
Lys	Ser	Asn	Val	Asp	Met	Val	Ser	Leu	Glu	Lys	Ser	Leu	Pro	Glu	Glu	
		230				235					240					
CTT	GTT	AAA	GAG	ATA	ATT	GAT	AGA	CGT	AAA	GAG	CTT	GGT	TTG	GAG	GTA	822
Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg	Arg	Lys	Glu	Leu	Gly	Leu	Glu	Val	
					250				255						260	
CCT	AAA	GTA	AAG	AAA	CAT	GTC	TCG	AAT	GTA	CAT	AAG	GCA	CTT	GAC	TCG	870
Pro	Lys	Val	Lys	Lys	His	Val	Ser	Asn	Val	His	Lys	Ala	Leu	Asp	Ser	
				265					270					275		
GAT	GAT	ATT	GAG	TTA	GTC	AAG	TTG	CTT	TTG	AAA	GAG	GAT	CAC	ACC	AAT	918
Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu	Leu	Leu	Lys	Glu	Asp	His	Thr	Asn	
			280					285					290			
CTA	GAT	GAT	GCG	TGT	GCT	CTT	CAT	TTC	GCT	GTT	GCA	TAT	TGC	AAT	GTG	966
Leu	Asp	Asp	Ala	Cys	Ala	Leu	His	Phe	Ala	Val	Ala	Tyr	Cys	Asn	Val	
			295				300					305				
AAG	ACC	GCA	ACA	GAT	CTT	TTA	AAA	CTT	GAT	CTT	GCC	GAT	GTC	AAC	CAT	1014
Lys	Thr	Ala	Thr	Asp	Leu	Leu	Lys	Leu	Asp	Leu	Ala	Asp	Val	Asn	His	
		310				315					320					
AGG	AAT	CCG	AGG	GGA	TAT	ACG	GTG	CTT	CAT	GTT	GCT	GCG	ATG	CGG	AAG	1062
Arg	Asn	Pro	Arg	Gly	Tyr	Thr	Val	Leu	His	Val	Ala	Ala	Met	Arg	Lys	
				330						335					340	
GAG	CCA	CAA	TTG	ATA	CTA	TCT	CTA	TTG	GAA	AAA	GGT	GCA	AGT	GCA	TCA	1110
Glu	Pro	Gln	Leu	Ile	Leu	Ser	Leu	Leu	Glu	Lys	Gly	Ala	Ser	Ala	Ser	
				345					350					355		
GAA	GCA	ACT	TTG	GAA	GGT	AGA	ACC	GCA	CTC	ATG	ATC	GCA	AAA	CAA	GCC	1158
Glu	Ala	Thr	Leu	Glu	Gly	Arg	Thr	Ala	Leu	Met	Ile	Ala	Lys	Gln	Ala	
			360					365					370			
ACT	ATG	GCG	GTT	GAA	TGT	AAT	AAT	ATC	CCG	GAG	CAA	TGC	AAG	CAT	TCT	1206
Thr	Met	Ala	Val	Glu	Cys	Asn	Asn	Ile	Pro	Glu	Gln	Cys	Lys	His	Ser	
			375				380					385				
CTC	AAA	GGC	CGA	CTA	TGT	GTA	GAA	ATA	CTA	GAG	CAA	GAA	GAC	AAA	CGA	1254
Leu	Lys	Gly	Arg	Leu	Cys	Val	Glu	Ile	Leu	Glu	Gln	Glu	Asp	Lys	Arg	
						395					400					
GAA	CAA	ATT	CCT	AGA	GAT	GTT	CCT	CCC	TCT	TTT	GCA	GTG	GCG	GCC	GAT	1302
Glu	Gln	Ile	Pro	Arg	Asp	Val	Pro	Pro	Ser	Phe	Ala	Val	Ala	Ala	Asp	
					410				415						420	
GAA	TTG	AAG	ATG	ACG	CTG	CTC	GAT	CTT	GAA	AAT	AGA	GTT	GCA	CTT	GCT	1350
Glu	Leu	Lys	Met	Thr	Leu	Leu	Asp	Leu	Glu	Asn	Arg	Val	Ala	Leu	Ala	
				425					430					435		

CAA CGT CTT TTT CCA ACG GAA GCA CAA GCT GCA ATG GAG ATC GCC GAA	1398
Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala Glu	
440 445 450	
ATG AAG GGA ACA TGT GAG TTC ATA GTG ACT AGC CTC GAG CCT GAC CGT	1446
Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp Arg	
455 460 465	
CTC ACT GGT ACG AAG AGA ACA TCA CCG GGT GTA AAG ATA GCA CCT TTC	1494
Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro Phe	
470 475 480	
AGA ATC CTA GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA ACC	1542
Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys Thr	
485 490 495 500	
GTG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC GAC	1590
Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu Asp	
505 510 515	
CAG ATT ATG AAC TGT GAG GAC TTG ACT CAA CTG GCT TGC GGA GAA GAC	1638
Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu Asp	
520 525 530	
GAC ACT GCT GAG AAA CGA CTA CAA AAG AAG CAA AGG TAC ATG GAA ATA	1686
Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu Ile	
535 540 545	
CAA GAG ACA CTA AAG AAG GCC TTT AGT GAG GAC AAT TTG GAA TTA GGA	1734
Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn Leu Glu Leu Gly	
550 555 560	
AAT TTG TCC CTG ACA GAT TCG ACT TCT TCC ACA TCG AAA TCA ACC GGT	1782
Asn Leu Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser Lys Ser Thr Gly	
565 570 575 580	
GGA AAG AGG TCT AAC CGT AAA CTC TCT CAT CGT CGT CGG TGA	1824
Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg Arg *	
585 590	
GACTCTTGCC TCTTAGTGTA ATTTTGTGCTG TACCATATAA TTCTGTTTTC ATGATGACTG	1884
TAAGTGTGTTA TGTCTATCGT TGGCGTCATA TAGTTTCGCT CTTCGTTTTG CATCCTGTGT	1944
ATTATTGCTG CAGGTGTGCT TCAAACAAAT GTTGTAACAA TTTGAACCAA TGGTATACAG	2004
ATTTGTA	2011

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2011 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 - (B) LOCATION: 43..1824
 - (D) OTHER INFORMATION: /product= "altered form of NIM1"
- /note= "Serine residues at amino acid positions 55 and 59 in

wild-type NIM1 gene product have been changed to Alanine residues."

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 205..217

(D) OTHER INFORMATION: /note= "nucleotides 205 and 217 changed from T's to G's compared to wild-type sequence."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATCTCTTTA ATTTGTGAAT TTCAATTCAT CGGAACCTGT TG ATG GAC ACC ACC	54
Met Asp Thr Thr	
1	
ATT GAT GGA TTC GCC GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC	102
Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val	
5 10 15 20	
GCT ACC GAT AAC ACC GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA	150
Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln	
25 30 35	
GTA CTC ACC GGA CCT GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC	198
Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser	
40 45 50	
TTC GAA GCC GTC TTT GAC GCG CCG GAT GAT TTC TAC AGC GAC GCT AAG	246
Phe Glu Ala Val Phe Asp Ala Pro Asp Asp Phe Tyr Ser Asp Ala Lys	
55 60 65	
CTT GTT CTC TCC GAC GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG	294
Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu	
70 75 80	
TCA GCG AGA AGC TCT TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG	342
Ser Ala Arg Ser Ser Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys	
85 90 95 100	
GAG AAA GAC TCC AAC AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG	390
Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu	
105 110 115	
ATT GCC AAG GAT TAC GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG	438
Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu	
120 125 130	
GCT TAT GTT TAC AGC AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT	486
Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser	
135 140 145	
GAA TGC GCA GAC GAG AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG	534
Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val	
150 155 160	
GAT TTC ATG TTG GAG GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT	582
Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro	
165 170 175 180	
GAA TTA ATT ACT CTC TAT CAG AGG CAC TTA TTG GAC GTT GTA GAC AAA	630
Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys	
185 190 195	
GTT GTT ATA GAG GAC ACA TTG GTT ATA CTC AAG CTT GCT AAT ATA TGT	678

10016236-12130

Val	Val	Ile	Glu	Asp	Thr	Leu	Val	Ile	Leu	Lys	Leu	Ala	Asn	Ile	Cys	
			200					205					210			
GGT	AAA	GCT	TGT	ATG	AAG	CTA	TTG	GAT	AGA	TGT	AAA	GAG	ATT	ATT	GTC	726
Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu	Asp	Arg	Cys	Lys	Glu	Ile	Ile	Val	
		215					220					225				
AAG	TCT	AAT	GTA	GAT	ATG	GTT	AGT	CTT	GAA	AAG	TCA	TTG	CCG	GAA	GAG	774
Lys	Ser	Asn	Val	Asp	Met	Val	Ser	Leu	Glu	Lys	Ser	Leu	Pro	Glu	Glu	
	230					235					240					
CTT	GTT	AAA	GAG	ATA	ATT	GAT	AGA	CGT	AAA	GAG	CTT	GGT	TTG	GAG	GTA	822
Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg	Arg	Lys	Glu	Leu	Gly	Leu	Glu	Val	
245					250					255					260	
CCT	AAA	GTA	AAG	AAA	CAT	GTC	TCG	AAT	GTA	CAT	AAG	GCA	CTT	GAC	TCG	870
Pro	Lys	Val	Lys	Lys	His	Val	Ser	Asn	Val	His	Lys	Ala	Leu	Asp	Ser	
				265					270					275		
GAT	GAT	ATT	GAG	TTA	GTC	AAG	TTG	CTT	TTG	AAA	GAG	GAT	CAC	ACC	AAT	918
Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu	Leu	Leu	Lys	Glu	Asp	His	Thr	Asn	
			280					285					290			
CTA	GAT	GAT	GCG	TGT	GCT	CTT	CAT	TTC	GCT	GTT	GCA	TAT	TGC	AAT	GTG	966
Leu	Asp	Asp	Ala	Cys	Ala	Leu	His	Phe	Ala	Val	Ala	Tyr	Cys	Asn	Val	
		295					300					305				
AAG	ACC	GCA	ACA	GAT	CTT	TTA	AAA	CTT	GAT	CTT	GCC	GAT	GTC	AAC	CAT	1014
Lys	Thr	Ala	Thr	Asp	Leu	Leu	Lys	Leu	Asp	Leu	Ala	Asp	Val	Asn	His	
	310					315					320					
AGG	AAT	CCG	AGG	GGA	TAT	ACG	GTG	CTT	CAT	GTT	GCT	GCG	ATG	CGG	AAG	1062
Arg	Asn	Pro	Arg	Gly	Tyr	Thr	Val	Leu	His	Val	Ala	Ala	Met	Arg	Lys	
325					330					335					340	
GAG	CCA	CAA	TTG	ATA	CTA	TCT	CTA	TTG	GAA	AAA	GGT	GCA	AGT	GCA	TCA	1110
Glu	Pro	Gln	Leu	Ile	Leu	Ser	Leu	Leu	Glu	Lys	Gly	Ala	Ser	Ala	Ser	
				345					350					355		
GAA	GCA	ACT	TTG	GAA	GGT	AGA	ACC	GCA	CTC	ATG	ATC	GCA	AAA	CAA	GCC	1158
Glu	Ala	Thr	Leu	Glu	Gly	Arg	Thr	Ala	Leu	Met	Ile	Ala	Lys	Gln	Ala	
			360					365					370			
ACT	ATG	GCG	GTT	GAA	TGT	AAT	AAT	ATC	CCG	GAG	CAA	TGC	AAG	CAT	TCT	1206
Thr	Met	Ala	Val	Glu	Cys	Asn	Asn	Ile	Pro	Glu	Gln	Cys	Lys	His	Ser	
		375					380					385				
CTC	AAA	GGC	CGA	CTA	TGT	GTA	GAA	ATA	CTA	GAG	CAA	GAA	GAC	AAA	CGA	1254
Leu	Lys	Gly	Arg	Leu	Cys	Val	Glu	Ile	Leu	Glu	Gln	Glu	Asp	Lys	Arg	
	390					395					400					
GAA	CAA	ATT	CCT	AGA	GAT	GTT	CCT	CCC	TCT	TTT	GCA	GTG	GCG	GCC	GAT	1302
Glu	Gln	Ile	Pro	Arg	Asp	Val	Pro	Pro	Ser	Phe	Ala	Val	Ala	Ala	Asp	
405					410					415					420	
GAA	TTG	AAG	ATG	ACG	CTG	CTC	GAT	CTT	GAA	AAT	AGA	GTT	GCA	CTT	GCT	1350
Glu	Leu	Lys	Met	Thr	Leu	Leu	Asp	Leu	Glu	Asn	Arg	Val	Ala	Leu	Ala	
				425					430					435		
CAA	CGT	CTT	TTT	CCA	ACG	GAA	GCA	CAA	GCT	GCA	ATG	GAG	ATC	GCC	GAA	1398
Gln	Arg	Leu	Phe	Pro	Thr	Glu	Ala	Gln	Ala	Ala	Met	Glu	Ile	Ala	Glu	
			440					445					450			
ATG	AAG	GGA	ACA	TGT	GAG	TTC	ATA	GTG	ACT	AGC	CTC	GAG	CCT	GAC	CGT	1446
Met	Lys	Gly	Thr	Cys	Glu	Phe	Ile	Val	Thr	Ser	Leu	Glu	Pro	Asp	Arg	

	455		460		465														
CTC	ACT	GGT	ACG	AAG	AGA	ACA	TCA	CCG	GGT	GTA	AAG	ATA	GCA	CCT	TTC				1494
Leu	Thr	Gly	Thr	Lys	Arg	Thr	Ser	Pro	Gly	Val	Lys	Ile	Ala	Pro	Phe				
	470						475				480								
AGA	ATC	CTA	GAA	GAG	CAT	CAA	AGT	AGA	CTA	AAA	GCG	CTT	TCT	AAA	ACC				1542
Arg	Ile	Leu	Glu	Glu	His	Gln	Ser	Arg	Leu	Lys	Ala	Leu	Ser	Lys	Thr				
	485					490				495					500				
GTG	GAA	CTC	GGG	AAA	CGA	TTC	TTC	CCG	CGC	TGT	TCG	GCA	GTG	CTC	GAC				1590
Val	Glu	Leu	Gly	Lys	Arg	Phe	Phe	Pro	Arg	Cys	Ser	Ala	Val	Leu	Asp				
				505					510					515					
CAG	ATT	ATG	AAC	TGT	GAG	GAC	TTG	ACT	CAA	CTG	GCT	TGC	GGA	GAA	GAC				1638
Gln	Ile	Met	Asn	Cys	Glu	Asp	Leu	Thr	Gln	Leu	Ala	Cys	Gly	Glu	Asp				
			520					525					530						
GAC	ACT	GCT	GAG	AAA	CGA	CTA	CAA	AAG	AAG	CAA	AGG	TAC	ATG	GAA	ATA				1686
Asp	Thr	Ala	Glu	Lys	Arg	Leu	Gln	Lys	Lys	Gln	Arg	Tyr	Met	Glu	Ile				
		535					540					545							
CAA	GAG	ACA	CTA	AAG	AAG	GCC	TTT	AGT	GAG	GAC	AAT	TTG	GAA	TTA	GGA				1734
Gln	Glu	Thr	Leu	Lys	Lys	Ala	Phe	Ser	Glu	Asp	Asn	Leu	Glu	Leu	Gly				
		550				555					560								
AAT	TTG	TCC	CTG	ACA	GAT	TCG	ACT	TCT	TCC	ACA	TCG	AAA	TCA	ACC	GGT				1782
Asn	Leu	Ser	Leu	Thr	Asp	Ser	Thr	Ser	Ser	Thr	Ser	Lys	Ser	Thr	Gly				
	565				570				575						580				
GGA	AAG	AGG	TCT	AAC	CGT	AAA	CTC	TCT	CAT	CGT	CGT	CGG	TGA						1824
Gly	Lys	Arg	Ser	Asn	Arg	Lys	Leu	Ser	His	Arg	Arg	Arg	*						
				585				590											
GACTCTTGCC	TCTTAGTGTA	ATTTTGTGCTG	TACCATATAA	TTCTGTTTTTC	ATGATGACTG														1884
TAAGTGTGTTA	TGTCTATCGT	TGGCGTCATA	TAGTTTCGCT	CTTCGTTTTG	CATCCTGTGT														1944
ATTATTGCTG	CAGGTGTGCT	TCAAACAAAT	GTTGTAACAA	TTTGAACCAA	TGGTATACAG														2004
ATTGTA																			2011

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Thr Thr Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser
1 5 10 15

Thr Ser Phe Val Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu
20 25 30

Ala Ala Glu Gln Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu
35 40 45

Leu Ser Asn Ser Phe Glu Ala Val Phe Asp Ala Pro Asp Asp Phe Tyr
50 55 60

Ser	Asp	Ala	Lys	Leu	Val	Leu	Ser	Asp	Gly	Arg	Glu	Val	Ser	Phe	His	
65					70					75					80	
Arg	Cys	Val	Leu	Ser	Ala	Arg	Ser	Ser	Phe	Phe	Lys	Ser	Ala	Leu	Ala	
				85					90					95		
Ala	Ala	Lys	Lys	Glu	Lys	Asp	Ser	Asn	Asn	Thr	Ala	Ala	Val	Lys	Leu	
			100					105					110			
Glu	Leu	Lys	Glu	Ile	Ala	Lys	Asp	Tyr	Glu	Val	Gly	Phe	Asp	Ser	Val	
		115					120					125				
Val	Thr	Val	Leu	Ala	Tyr	Val	Tyr	Ser	Ser	Arg	Val	Arg	Pro	Pro	Pro	
	130					135					140					
Lys	Gly	Val	Ser	Glu	Cys	Ala	Asp	Glu	Asn	Cys	Cys	His	Val	Ala	Cys	
145					150					155					160	
Arg	Pro	Ala	Val	Asp	Phe	Met	Leu	Glu	Val	Leu	Tyr	Leu	Ala	Phe	Ile	
				165					170					175		
Phe	Lys	Ile	Pro	Glu	Leu	Ile	Thr	Leu	Tyr	Gln	Arg	His	Leu	Leu	Asp	
			180					185					190			
Val	Val	Asp	Lys	Val	Val	Ile	Glu	Asp	Thr	Leu	Val	Ile	Leu	Lys	Leu	
		195					200					205				
Ala	Asn	Ile	Cys	Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu	Asp	Arg	Cys	Lys	
	210					215					220					
Glu	Ile	Ile	Val	Lys	Ser	Asn	Val	Asp	Met	Val	Ser	Leu	Glu	Lys	Ser	
225					230					235					240	
Leu	Pro	Glu	Glu	Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg	Arg	Lys	Glu	Leu	
				245					250					255		
Gly	Leu	Glu	Val	Pro	Lys	Val	Lys	Lys	His	Val	Ser	Asn	Val	His	Lys	
			260					265					270			
Ala	Leu	Asp	Ser	Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu	Leu	Leu	Lys	Glu	
		275					280					285				
Asp	His	Thr	Asn	Leu	Asp	Asp	Ala	Cys	Ala	Leu	His	Phe	Ala	Val	Ala	
	290					295					300					
Tyr	Cys	Asn	Val	Lys	Thr	Ala	Thr	Asp	Leu	Leu	Lys	Leu	Asp	Leu	Ala	
305					310					315					320	
Asp	Val	Asn	His	Arg	Asn	Pro	Arg	Gly	Tyr	Thr	Val	Leu	His	Val	Ala	
				325					330					335		
Ala	Met	Arg	Lys	Glu	Pro	Gln	Leu	Ile	Leu	Ser	Leu	Leu	Glu	Lys	Gly	
			340					345					350			
Ala	Ser	Ala	Ser	Glu	Ala	Thr	Leu	Glu	Gly	Arg	Thr	Ala	Leu	Met	Ile	
		355					360					365				
Ala	Lys	Gln	Ala	Thr	Met	Ala	Val	Glu	Cys	Asn	Asn	Ile	Pro	Glu	Gln	
	370					375					380					
Cys	Lys	His	Ser	Leu	Lys	Gly	Arg	Leu	Cys	Val	Glu	Ile	Leu	Glu	Gln	
385					390					395					400	
Glu	Asp	Lys	Arg	Glu	Gln	Ile	Pro	Arg	Asp	Val	Pro	Pro	Ser	Phe	Ala	

405					410					415					
Val	Ala	Ala	Asp	Glu	Leu	Lys	Met	Thr	Leu	Leu	Asp	Leu	Glu	Asn	Arg
			420					425					430		
Val	Ala	Leu	Ala	Gln	Arg	Leu	Phe	Pro	Thr	Glu	Ala	Gln	Ala	Ala	Met
		435					440					445			
Glu	Ile	Ala	Glu	Met	Lys	Gly	Thr	Cys	Glu	Phe	Ile	Val	Thr	Ser	Leu
	450					455					460				
Glu	Pro	Asp	Arg	Leu	Thr	Gly	Thr	Lys	Arg	Thr	Ser	Pro	Gly	Val	Lys
465						470					475				480
Ile	Ala	Pro	Phe	Arg	Ile	Leu	Glu	Glu	His	Gln	Ser	Arg	Leu	Lys	Ala
				485					490						495
Leu	Ser	Lys	Thr	Val	Glu	Leu	Gly	Lys	Arg	Phe	Phe	Pro	Arg	Cys	Ser
			500					505					510		
Ala	Val	Leu	Asp	Gln	Ile	Met	Asn	Cys	Glu	Asp	Leu	Thr	Gln	Leu	Ala
		515					520					525			
Cys	Gly	Glu	Asp	Asp	Thr	Ala	Glu	Lys	Arg	Leu	Gln	Lys	Lys	Gln	Arg
	530					535					540				
Tyr	Met	Glu	Ile	Gln	Glu	Thr	Leu	Lys	Lys	Ala	Phe	Ser	Glu	Asp	Asn
545						550					555				560
Leu	Glu	Leu	Gly	Asn	Leu	Ser	Leu	Thr	Asp	Ser	Thr	Ser	Ser	Thr	Ser
				565					570					575	
Lys	Ser	Thr	Gly	Gly	Lys	Arg	Ser	Asn	Arg	Lys	Leu	Ser	His	Arg	Arg
			580					585					590		
Arg	*														

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1410
 - (D) OTHER INFORMATION: /product= "Altered form of NIM1"
- /note= "N-terminal deletion compared to wild-type NIM1 sequence."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG	GAT	TCG	GTT	GTG	ACT	GTT	TTG	GCT	TAT	GTT	TAC	AGC	AGC	AGA	GTG	48
Met	Asp	Ser	Val	Val	Thr	Val	Leu	Ala	Tyr	Val	Tyr	Ser	Ser	Arg	Val	
1				5				10						15		
AGA	CCG	CCG	CCT	AAA	GGA	GTT	TCT	GAA	TGC	GCA	GAC	GAG	AAT	TGC	TGC	96
Arg	Pro	Pro	Pro	Lys	Gly	Val	Ser	Glu	Cys	Ala	Asp	Glu	Asn	Cys	Cys	

				20				25				30							
CAC	GTG	GCT	TGC	CGG	CCG	GCG	GTG	GAT	TTC	ATG	TTG	GAG	GTT	CTC	TAT		144		
His	Val	Ala	Cys	Arg	Pro	Ala	Val	Asp	Phe	Met	Leu	Glu	Val	Leu	Tyr				
				35				40				45							
TTG	GCT	TTC	ATC	TTC	AAG	ATC	CCT	GAA	TTA	ATT	ACT	CTC	TAT	CAG	AGG		192		
Leu	Ala	Phe	Ile	Phe	Lys	Ile	Pro	Glu	Leu	Ile	Thr	Leu	Tyr	Gln	Arg				
				50				55				60							
CAC	TTA	TTG	GAC	GTT	GTA	GAC	AAA	GTT	GTT	ATA	GAG	GAC	ACA	TTG	GTT		240		
His	Leu	Leu	Asp	Val	Val	Asp	Lys	Val	Val	Ile	Glu	Asp	Thr	Leu	Val				
				70				75								80			
ATA	CTC	AAG	CTT	GCT	AAT	ATA	TGT	GGT	AAA	GCT	TGT	ATG	AAG	CTA	TTG		288		
Ile	Leu	Lys	Leu	Ala	Asn	Ile	Cys	Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu				
				85				90								95			
GAT	AGA	TGT	AAA	GAG	ATT	ATT	GTC	AAG	TCT	AAT	GTA	GAT	ATG	GTT	AGT		336		
Asp	Arg	Cys	Lys	Glu	Ile	Ile	Val	Lys	Ser	Asn	Val	Asp	Met	Val	Ser				
				100				105				110							
CTT	GAA	AAG	TCA	TTG	CCG	GAA	GAG	CTT	GTT	AAA	GAG	ATA	ATT	GAT	AGA		384		
Leu	Glu	Lys	Ser	Leu	Pro	Glu	Glu	Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg				
				115				120				125							
CGT	AAA	GAG	CTT	GGT	TTG	GAG	GTA	CCT	AAA	GTA	AAG	AAA	CAT	GTC	TCG		432		
Arg	Lys	Glu	Leu	Gly	Leu	Glu	Val	Pro	Lys	Val	Lys	Lys	His	Val	Ser				
				130				135				140							
AAT	GTA	CAT	AAG	GCA	CTT	GAC	TCG	GAT	GAT	ATT	GAG	TTA	GTC	AAG	TTG		480		
Asn	Val	His	Lys	Ala	Leu	Asp	Ser	Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu				
				145				150				155				160			
CTT	TTG	AAA	GAG	GAT	CAC	ACC	AAT	CTA	GAT	GAT	GCG	TGT	GCT	CTT	CAT		528		
Leu	Leu	Lys	Glu	Asp	His	Thr	Asn	Leu	Asp	Asp	Ala	Cys	Ala	Leu	His				
				165				170				175							
TTC	GCT	GTT	GCA	TAT	TGC	AAT	GTG	AAG	ACC	GCA	ACA	GAT	CTT	TTA	AAA		576		
Phe	Ala	Val	Ala	Tyr	Cys	Asn	Val	Lys	Thr	Ala	Thr	Asp	Leu	Leu	Lys				
				180				185				190							
CTT	GAT	CTT	GCC	GAT	GTC	AAC	CAT	AGG	AAT	CCG	AGG	GGA	TAT	ACG	GTG		624		
Leu	Asp	Leu	Ala	Asp	Val	Asn	His	Arg	Asn	Pro	Arg	Gly	Tyr	Thr	Val				
				195				200				205							
CTT	CAT	GTT	GCT	GCG	ATG	CGG	AAG	GAG	CCA	CAA	TTG	ATA	CTA	TCT	CTA		672		
Leu	His	Val	Ala	Ala	Met	Arg	Lys	Glu	Pro	Gln	Leu	Ile	Leu	Ser	Leu				
				210				215				220							
TTG	GAA	AAA	GGT	GCA	AGT	GCA	TCA	GAA	GCA	ACT	TTG	GAA	GGT	AGA	ACC		720		
Leu	Glu	Lys	Gly	Ala	Ser	Ala	Ser	Glu	Ala	Thr	Leu	Glu	Gly	Arg	Thr				
				225				230				235				240			
GCA	CTC	ATG	ATC	GCA	AAA	CAA	GCC	ACT	ATG	GCG	GTT	GAA	TGT	AAT	AAT		768		
Ala	Leu	Met	Ile	Ala	Lys	Gln	Ala	Thr	Met	Ala	Val	Glu	Cys	Asn	Asn				
				245				250				255							
ATC	CCG	GAG	CAA	TGC	AAG	CAT	TCT	CTC	AAA	GGC	CGA	CTA	TGT	GTA	GAA		816		
Ile	Pro	Glu	Gln	Cys	Lys	His	Ser	Leu	Lys	Gly	Arg	Leu	Cys	Val	Glu				
				260				265				270							
ATA	CTA	GAG	CAA	GAA	GAC	AAA	CGA	GAA	CAA	ATT	CCT	AGA	GAT	GTT	CCT		864		
Ile	Leu	Glu	Gln	Glu	Asp	Lys	Arg	Glu	Gln	Ile	Pro	Arg	Asp	Val	Pro				
				275				280				285							

CCC TCT TTT GCA GTG GCG GCC GAT GAA TTG AAG ATG ACG CTG CTC GAT	912
Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp	
290 295 300	
CTT GAA AAT AGA GTT GCA CTT GCT CAA CGT CTT TTT CCA ACG GAA GCA	960
Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala	
305 310 315 320	
CAA GCT GCA ATG GAG ATC GCC GAA ATG AAG GGA ACA TGT GAG TTC ATA	1008
Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile	
325 330 335	
GTG ACT AGC CTC GAG CCT GAC CGT CTC ACT GGT ACG AAG AGA ACA TCA	1056
Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser	
340 345 350	
CCG GGT GTA AAG ATA GCA CCT TTC AGA ATC CTA GAA GAG CAT CAA AGT	1104
Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser	
355 360 365	
AGA CTA AAA GCG CTT TCT AAA ACC GTG GAA CTC GGG AAA CGA TTC TTC	1152
Arg Leu Lys Ala Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe	
370 375 380	
CCG CGC TGT TCG GCA GTG CTC GAC CAG ATT ATG AAC TGT GAG GAC TTG	1200
Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met Asn Cys Glu Asp Leu	
385 390 395 400	
ACT CAA CTG GCT TGC GGA GAA GAC GAC ACT GCT GAG AAA CGA CTA CAA	1248
Thr Gln Leu Ala Cys Gly Glu Asp Asp Thr Ala Glu Lys Arg Leu Gln	
405 410 415	
AAG AAG CAA AGG TAC ATG GAA ATA CAA GAG ACA CTA AAG AAG GCC TTT	1296
Lys Lys Gln Arg Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys Ala Phe	
420 425 430	
AGT GAG GAC AAT TTG GAA TTA GGA AAT TTG TCC CTG ACA GAT TCG ACT	1344
Ser Glu Asp Asn Leu Glu Leu Gly Asn Leu Ser Leu Thr Asp Ser Thr	
435 440 445	
TCT TCC ACA TCG AAA TCA ACC GGT GGA AAG AGG TCT AAC CGT AAA CTC	1392
Ser Ser Thr Ser Lys Ser Thr Gly Gly Lys Arg Ser Asn Arg Lys Leu	
450 455 460	
TCT CAT CGT CGT CGG TGA GACTCTTGCC TCTTAGTGTA ATTTTGTCTG	1440
Ser His Arg Arg Arg *	
465 470	
TACCATATAA TTCTGTTTTT ATGATGACTG TAACGTGTTTA TGTCTATCGT TGGCGTCATA	1500
TAGTTTCGCT CTTCGTTTTG CATCCTGTGT ATTATTGCTG CAGGTGTGCT TCAAACAAAT	1560
GTTGTAACAA TTTGAACCAA TGGTATACAG ATTTGTA	1597

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Asp	Ser	Val	Val	Thr	Val	Leu	Ala	Tyr	Val	Tyr	Ser	Ser	Arg	Val
1				5					10					15	
Arg	Pro	Pro	Pro	Lys	Gly	Val	Ser	Glu	Cys	Ala	Asp	Glu	Asn	Cys	Cys
			20					25					30		
His	Val	Ala	Cys	Arg	Pro	Ala	Val	Asp	Phe	Met	Leu	Glu	Val	Leu	Tyr
		35					40					45			
Leu	Ala	Phe	Ile	Phe	Lys	Ile	Pro	Glu	Leu	Ile	Thr	Leu	Tyr	Gln	Arg
	50					55					60				
His	Leu	Leu	Asp	Val	Val	Asp	Lys	Val	Val	Ile	Glu	Asp	Thr	Leu	Val
65					70					75					80
Ile	Leu	Lys	Leu	Ala	Asn	Ile	Cys	Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu
				85					90					95	
Asp	Arg	Cys	Lys	Glu	Ile	Ile	Val	Lys	Ser	Asn	Val	Asp	Met	Val	Ser
			100					105					110		
Leu	Glu	Lys	Ser	Leu	Pro	Glu	Glu	Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg
		115					120					125			
Arg	Lys	Glu	Leu	Gly	Leu	Glu	Val	Pro	Lys	Val	Lys	Lys	His	Val	Ser
	130					135					140				
Asn	Val	His	Lys	Ala	Leu	Asp	Ser	Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu
145					150					155					160
Leu	Leu	Lys	Glu	Asp	His	Thr	Asn	Leu	Asp	Asp	Ala	Cys	Ala	Leu	His
				165					170					175	
Phe	Ala	Val	Ala	Tyr	Cys	Asn	Val	Lys	Thr	Ala	Thr	Asp	Leu	Leu	Lys
			180					185					190		
Leu	Asp	Leu	Ala	Asp	Val	Asn	His	Arg	Asn	Pro	Arg	Gly	Tyr	Thr	Val
	195						200					205			
Leu	His	Val	Ala	Ala	Met	Arg	Lys	Glu	Pro	Gln	Leu	Ile	Leu	Ser	Leu
	210					215					220				
Leu	Glu	Lys	Gly	Ala	Ser	Ala	Ser	Glu	Ala	Thr	Leu	Glu	Gly	Arg	Thr
225					230					235					240
Ala	Leu	Met	Ile	Ala	Lys	Gln	Ala	Thr	Met	Ala	Val	Glu	Cys	Asn	Asn
				245					250					255	
Ile	Pro	Glu	Gln	Cys	Lys	His	Ser	Leu	Lys	Gly	Arg	Leu	Cys	Val	Glu
			260					265					270		
Ile	Leu	Glu	Gln	Glu	Asp	Lys	Arg	Glu	Gln	Ile	Pro	Arg	Asp	Val	Pro
	275						280					285			
Pro	Ser	Phe	Ala	Val	Ala	Ala	Asp	Glu	Leu	Lys	Met	Thr	Leu	Leu	Asp
	290					295					300				
Leu	Glu	Asn	Arg	Val	Ala	Leu	Ala	Gln	Arg	Leu	Phe	Pro	Thr	Glu	Ala
305					310					315					320
Gln	Ala	Ala	Met	Glu	Ile	Ala	Glu	Met	Lys	Gly	Thr	Cys	Glu	Phe	Ile
				325					330					335	

10016336.121201

Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser
340 345 350
Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser
355 360 365
Arg Leu Lys Ala Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe
370 375 380
Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met Asn Cys Glu Asp Leu
385 390 395 400
Thr Gln Leu Ala Cys Gly Glu Asp Asp Thr Ala Glu Lys Arg Leu Gln
405 410 415
Lys Lys Gln Arg Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys Ala Phe
420 425 430
Ser Glu Asp Asn Leu Glu Leu Gly Asn Leu Ser Leu Thr Asp Ser Thr
435 440 445
Ser Ser Thr Ser Lys Ser Thr Gly Gly Lys Arg Ser Asn Arg Lys Leu
450 455 460
Ser His Arg Arg Arg *
465 470

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 - (B) LOCATION: 43..1608
 - (D) OTHER INFORMATION: /product= "Altered form of NIM1"
- /note= "C-terminal deletion compared to wild-type NIM1."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCTCTTTA ATTTGTGAAT TTCAATTCAT CGGAACCTGT TG ATG GAC ACC ACC	54
Met Asp Thr Thr	
1	
ATT GAT GGA TTC GCC GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC	102
Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val	
5 10 15 20	
GCT ACC GAT AAC ACC GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA	150
Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln	
25 30 35	
GTA CTC ACC GGA CCT GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC	198
Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser	
40 45 50	
TTC GAA TCC GTC TTT GAC TCG CCG GAT GAT TTC TAC AGC GAC GCT AAG	246
Phe Glu Ser Val Phe Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys	

55	60	65	
CTT GTT CTC TCC GAC GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu 70 75 80			294
TCA GCG AGA AGC TCT TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG Ser Ala Arg Ser Ser Phe Lys Ser Ala Leu Ala Ala Ala Lys Lys 85 90 95 100			342
GAG AAA GAC TCC AAC AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu 105 110 115			390
ATT GCC AAG GAT TAC GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu 120 125 130			438
GCT TAT GTT TAC AGC AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser 135 140 145			486
GAA TGC GCA GAC GAG AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val 150 155 160			534
GAT TTC ATG TTG GAG GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro 165 170 175 180			582
GAA TTA ATT ACT CTC TAT CAG AGG CAC TTA TTG GAC GTT GTA GAC AAA Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys 185 190 195			630
GTT GTT ATA GAG GAC ACA TTG GTT ATA CTC AAG CTT GCT AAT ATA TGT Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys 200 205 210			678
GGT AAA GCT TGT ATG AAG CTA TTG GAT AGA TGT AAA GAG ATT ATT GTC Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val 215 220 225			726
AAG TCT AAT GTA GAT ATG GTT AGT CTT GAA AAG TCA TTG CCG GAA GAG Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu 230 235 240			774
CTT GTT AAA GAG ATA ATT GAT AGA CGT AAA GAG CTT GGT TTG GAG GTA Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val 245 250 255 260			822
CCT AAA GTA AAG AAA CAT GTC TCG AAT GTA CAT AAG GCA CTT GAC TCG Pro Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser 265 270 275			870
GAT GAT ATT GAG TTA GTC AAG TTG CTT TTG AAA GAG GAT CAC ACC AAT Asp Asp Ile Glu Leu Val Lys Leu Leu Lys Glu Asp His Thr Asn 280 285 290			918
CTA GAT GAT GCG TGT GCT CTT CAT TTC GCT GTT GCA TAT TGC AAT GTG Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val 295 300 305			966
AAG ACC GCA ACA GAT CTT TTA AAA CTT GAT CTT GCC GAT GTC AAC CAT Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His 310 315 320			1014

AGG AAT CCG AGG GGA TAT ACG GTG CTT CAT GTT GCT GCG ATG CGG AAG	1062
Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Met Arg Lys	
325 330 335 340	
GAG CCA CAA TTG ATA CTA TCT CTA TTG GAA AAA GGT GCA AGT GCA TCA	1110
Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala Ser	
345 350 355	
GAA GCA ACT TTG GAA GGT AGA ACC GCA CTC ATG ATC GCA AAA CAA GCC	1158
Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln Ala	
360 365 370	
ACT ATG GCG GTT GAA TGT AAT AAT ATC CCG GAG CAA TGC AAG CAT TCT	1206
Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His Ser	
375 380 385	
CTC AAA GGC CGA CTA TGT GTA GAA ATA CTA GAG CAA GAA GAC AAA CGA	1254
Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys Arg	
390 395 400	
GAA CAA ATT CCT AGA GAT GTT CCT CCC TCT TTT GCA GTG GCG GCC GAT	1302
Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala Asp	
405 410 415 420	
GAA TTG AAG ATG ACG CTG CTC GAT CTT GAA AAT AGA GTT GCA CTT GCT	1350
Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg Val Ala Leu Ala	
425 430 435	
CAA CGT CTT TTT CCA ACG GAA GCA CAA GCT GCA ATG GAG ATC GCC GAA	1398
Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala Glu	
440 445 450	
ATG AAG GGA ACA TGT GAG TTC ATA GTG ACT AGC CTC GAG CCT GAC CGT	1446
Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp Arg	
455 460 465	
CTC ACT GGT ACG AAG AGA ACA TCA CCG GGT GTA AAG ATA GCA CCT TTC	1494
Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys Ile Ala Pro Phe	
470 475 480	
AGA ATC CTA GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA ACC	1542
Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala Leu Ser Lys Thr	
485 490 495 500	
GTG GAA CTC GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC GAC	1590
Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu Asp	
505 510 515	
CAG ATT ATG AAC TGT TGA	1608
Gln Ile Met Asn Cys *	
520	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Asp	Thr	Thr	Ile	Asp	Gly	Phe	Ala	Asp	Ser	Tyr	Glu	Ile	Ser	Ser	1	5	10	15
Thr	Ser	Phe	Val	Ala	Thr	Asp	Asn	Thr	Asp	Ser	Ser	Ile	Val	Tyr	Leu	20	25	30	
Ala	Ala	Glu	Gln	Val	Leu	Thr	Gly	Pro	Asp	Val	Ser	Ala	Leu	Gln	Leu	35	40	45	
Leu	Ser	Asn	Ser	Phe	Glu	Ser	Val	Phe	Asp	Ser	Pro	Asp	Asp	Phe	Tyr	50	55	60	
Ser	Asp	Ala	Lys	Leu	Val	Leu	Ser	Asp	Gly	Arg	Glu	Val	Ser	Phe	His	65	70	75	80
Arg	Cys	Val	Leu	Ser	Ala	Arg	Ser	Ser	Phe	Phe	Lys	Ser	Ala	Leu	Ala	85	90	95	
Ala	Ala	Lys	Lys	Glu	Lys	Asp	Ser	Asn	Asn	Thr	Ala	Ala	Val	Lys	Leu	100	105	110	
Glu	Leu	Lys	Glu	Ile	Ala	Lys	Asp	Tyr	Glu	Val	Gly	Phe	Asp	Ser	Val	115	120	125	
Val	Thr	Val	Leu	Ala	Tyr	Val	Tyr	Ser	Ser	Arg	Val	Arg	Pro	Pro	Pro	130	135	140	
Lys	Gly	Val	Ser	Glu	Cys	Ala	Asp	Glu	Asn	Cys	Cys	His	Val	Ala	Cys	145	150	155	160
Arg	Pro	Ala	Val	Asp	Phe	Met	Leu	Glu	Val	Leu	Tyr	Leu	Ala	Phe	Ile	165	170	175	
Phe	Lys	Ile	Pro	Glu	Leu	Ile	Thr	Leu	Tyr	Gln	Arg	His	Leu	Leu	Asp	180	185	190	
Val	Val	Asp	Lys	Val	Val	Ile	Glu	Asp	Thr	Leu	Val	Ile	Leu	Lys	Leu	195	200	205	
Ala	Asn	Ile	Cys	Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu	Asp	Arg	Cys	Lys	210	215	220	
Glu	Ile	Ile	Val	Lys	Ser	Asn	Val	Asp	Met	Val	Ser	Leu	Glu	Lys	Ser	225	230	235	240
Leu	Pro	Glu	Glu	Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg	Arg	Lys	Glu	Leu	245	250	255	
Gly	Leu	Glu	Val	Pro	Lys	Val	Lys	Lys	His	Val	Ser	Asn	Val	His	Lys	260	265	270	
Ala	Leu	Asp	Ser	Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu	Leu	Leu	Lys	Glu	275	280	285	
Asp	His	Thr	Asn	Leu	Asp	Asp	Ala	Cys	Ala	Leu	His	Phe	Ala	Val	Ala	290	295	300	
Tyr	Cys	Asn	Val	Lys	Thr	Ala	Thr	Asp	Leu	Leu	Lys	Leu	Asp	Leu	Ala	305	310	315	320
Asp	Val	Asn	His	Arg	Asn	Pro	Arg	Gly	Tyr	Thr	Val	Leu	His	Val	Ala	325	330	335	
Ala	Met	Arg	Lys	Glu	Pro	Gln	Leu	Ile	Leu	Ser	Leu	Leu	Glu	Lys	Gly	340	345	350	

Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile
 355 360 365

Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln
 370 375 380

Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln
 385 390 395 400

Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala
 405 410 415

Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg
 420 425 430

Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met
 435 440 445

Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu
 450 455 460

Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys
 465 470 475 480

Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala
 485 490 495

Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser
 500 505 510

Ala Val Leu Asp Gln Ile Met Asn Cys *
 515 520

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1194
 - (D) OTHER INFORMATION: /product= "Altered form of NIM1"
- /note= "N-terminal/C-terminal chimera."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GAT TCG GTT GTG ACT GTT TTG GCT TAT GTT TAC AGC AGC AGA GTG	48
Met Asp Ser Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val	
1 5 10 15	
AGA CCG CCG CCT AAA GGA GTT TCT GAA TGC GCA GAC GAG AAT TGC TGC	96
Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys	
20 25 30	
CAC GTG GCT TGC CGG CCG GCG GTG GAT TTC ATG TTG GAG GTT CTC TAT	144
His Val Ala Cys Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr	
35 40 45	

TTG	GCT	TTC	ATC	TTC	AAG	ATC	CCT	GAA	TTA	ATT	ACT	CTC	TAT	CAG	AGG	192
Leu	Ala	Phe	Ile	Phe	Lys	Ile	Pro	Glu	Leu	Ile	Thr	Leu	Tyr	Gln	Arg	
	50					55					60					
CAC	TTA	TTG	GAC	GTT	GTA	GAC	AAA	GTT	GTT	ATA	GAG	GAC	ACA	TTG	GTT	240
His	Leu	Leu	Asp	Val	Val	Asp	Lys	Val	Val	Ile	Glu	Asp	Thr	Leu	Val	
	65				70					75					80	
ATA	CTC	AAG	CTT	GCT	AAT	ATA	TGT	GGT	AAA	GCT	TGT	ATG	AAG	CTA	TTG	288
Ile	Leu	Lys	Leu	Ala	Asn	Ile	Cys	Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu	
				85					90					95		
GAT	AGA	TGT	AAA	GAG	ATT	ATT	GTC	AAG	TCT	AAT	GTA	GAT	ATG	GTT	AGT	336
Asp	Arg	Cys	Lys	Glu	Ile	Ile	Val	Lys	Ser	Asn	Val	Asp	Met	Val	Ser	
			100					105					110			
CTT	GAA	AAG	TCA	TTG	CCG	GAA	GAG	CTT	GTT	AAA	GAG	ATA	ATT	GAT	AGA	384
Leu	Glu	Lys	Ser	Leu	Pro	Glu	Glu	Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg	
		115					120					125				
CGT	AAA	GAG	CTT	GGT	TTG	GAG	GTA	CCT	AAA	GTA	AAG	AAA	CAT	GTC	TCG	432
Arg	Lys	Glu	Leu	Gly	Leu	Glu	Val	Pro	Lys	Val	Lys	Lys	His	Val	Ser	
	130					135					140					
AAT	GTA	CAT	AAG	GCA	CTT	GAC	TCG	GAT	GAT	ATT	GAG	TTA	GTC	AAG	TTG	480
Asn	Val	His	Lys	Ala	Leu	Asp	Ser	Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu	
	145				150					155					160	
CTT	TTG	AAA	GAG	GAT	CAC	ACC	AAT	CTA	GAT	GAT	GCG	TGT	GCT	CTT	CAT	528
Leu	Leu	Lys	Glu	Asp	His	Thr	Asn	Leu	Asp	Asp	Ala	Cys	Ala	Leu	His	
				165					170					175		
TTC	GCT	GTT	GCA	TAT	TGC	AAT	GTG	AAG	ACC	GCA	ACA	GAT	CTT	TTA	AAA	576
Phe	Ala	Val	Ala	Tyr	Cys	Asn	Val	Lys	Thr	Ala	Thr	Asp	Leu	Leu	Lys	
			180					185					190			
CTT	GAT	CTT	GCC	GAT	GTC	AAC	CAT	AGG	AAT	CCG	AGG	GGA	TAT	ACG	GTG	624
Leu	Asp	Leu	Ala	Asp	Val	Asn	His	Arg	Asn	Pro	Arg	Gly	Tyr	Thr	Val	
		195					200					205				
CTT	CAT	GTT	GCT	GCG	ATG	CGG	AAG	GAG	CCA	CAA	TTG	ATA	CTA	TCT	CTA	672
Leu	His	Val	Ala	Ala	Met	Arg	Lys	Glu	Pro	Gln	Leu	Ile	Leu	Ser	Leu	
	210					215					220					
TTG	GAA	AAA	GGT	GCA	AGT	GCA	TCA	GAA	GCA	ACT	TTG	GAA	GGT	AGA	ACC	720
Leu	Glu	Lys	Gly	Ala	Ser	Ala	Ser	Glu	Ala	Thr	Leu	Glu	Gly	Arg	Thr	
	225				230					235					240	
GCA	CTC	ATG	ATC	GCA	AAA	CAA	GCC	ACT	ATG	GCG	GTT	GAA	TGT	AAT	AAT	768
Ala	Leu	Met	Ile	Ala	Lys	Gln	Ala	Thr	Met	Ala	Val	Glu	Cys	Asn	Asn	
				245					250					255		
ATC	CCG	GAG	CAA	TGC	AAG	CAT	TCT	CTC	AAA	GGC	CGA	CTA	TGT	GTA	GAA	816
Ile	Pro	Glu	Gln	Cys	Lys	His	Ser	Leu	Lys	Gly	Arg	Leu	Cys	Val	Glu	
			260					265					270			
ATA	CTA	GAG	CAA	GAA	GAC	AAA	CGA	GAA	CAA	ATT	CCT	AGA	GAT	GTT	CCT	864
Ile	Leu	Glu	Gln	Glu	Asp	Lys	Arg	Glu	Gln	Ile	Pro	Arg	Asp	Val	Pro	
		275					280					285				
CCC	TCT	TTT	GCA	GTG	GCG	GCC	GAT	GAA	TTG	AAG	ATG	ACG	CTG	CTC	GAT	912
Pro	Ser	Phe	Ala	Val	Ala	Ala	Asp	Glu	Leu	Lys	Met	Thr	Leu	Leu	Asp	
	290					295					300					

CTT GAA AAT AGA GTT GCA CTT GCT CAA CGT CTT TTT CCA ACG GAA GCA	960
Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala	
305 310 315 320	
CAA GCT GCA ATG GAG ATC GCC GAA ATG AAG GGA ACA TGT GAG TTC ATA	1008
Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile	
325 330 335	
GTG ACT AGC CTC GAG CCT GAC CGT CTC ACT GGT ACG AAG AGA ACA TCA	1056
Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser	
340 345 350	
CCG GGT GTA AAG ATA GCA CCT TTC AGA ATC CTA GAA GAG CAT CAA AGT	1104
Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser	
355 360 365	
AGA CTA AAA GCG CTT TCT AAA ACC GTG GAA CTC GGG AAA CGA TTC TTC	1152
Arg Leu Lys Ala Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe	
370 375 380	
CCG CGC TGT TCG GCA GTG CTC GAC CAG ATT ATG AAC TGT TGA	1194
Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met Asn Cys *	
385 390 395	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Asp	Ser	Val	Val	Thr	Val	Leu	Ala	Tyr	Val	Tyr	Ser	Ser	Arg	Val
1				5					10					15	
Arg	Pro	Pro	Pro	Lys	Gly	Val	Ser	Glu	Cys	Ala	Asp	Glu	Asn	Cys	Cys
			20					25					30		
His	Val	Ala	Cys	Arg	Pro	Ala	Val	Asp	Phe	Met	Leu	Glu	Val	Leu	Tyr
		35					40					45			
Leu	Ala	Phe	Ile	Phe	Lys	Ile	Pro	Glu	Leu	Ile	Thr	Leu	Tyr	Gln	Arg
	50					55					60				
His	Leu	Leu	Asp	Val	Val	Asp	Lys	Val	Val	Ile	Glu	Asp	Thr	Leu	Val
65				70						75				80	
Ile	Leu	Lys	Leu	Ala	Asn	Ile	Cys	Gly	Lys	Ala	Cys	Met	Lys	Leu	Leu
				85					90					95	
Asp	Arg	Cys	Lys	Glu	Ile	Ile	Val	Lys	Ser	Asn	Val	Asp	Met	Val	Ser
			100					105					110		
Leu	Glu	Lys	Ser	Leu	Pro	Glu	Glu	Leu	Val	Lys	Glu	Ile	Ile	Asp	Arg
		115					120					125			
Arg	Lys	Glu	Leu	Gly	Leu	Glu	Val	Pro	Lys	Val	Lys	Lys	His	Val	Ser
	130					135					140				
Asn	Val	His	Lys	Ala	Leu	Asp	Ser	Asp	Asp	Ile	Glu	Leu	Val	Lys	Leu
145					150					155					160

Leu Leu Lys Glu Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His
 165 170 175

Phe Ala Val Ala Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys
 180 185 190

Leu Asp Leu Ala Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val
 195 200 205

Leu His Val Ala Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu
 210 215 220

Leu Glu Lys Gly Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr
 225 230 235 240

Ala Leu Met Ile Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn
 245 250 255

Ile Pro Glu Gln Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu
 260 265 270

Ile Leu Glu Gln Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro
 275 280 285

Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp
 290 295 300

Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala
 305 310 315 320

Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile
 325 330 335

Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser
 340 345 350

Pro Gly Val Lys Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser
 355 360 365

Arg Leu Lys Ala Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe
 370 375 380

Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met Asn Cys *
 385 390 395

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 786 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..786
 (D) OTHER INFORMATION: /product= "Altered form of NIM1"
 /note= "Ankyrin domains of NIM1."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATG Met 1	GAC Asp	TCC Ser	AAC Asn	AAC Asn 5	ACC Thr	GCC Ala	GCC Ala	GTG Val	AAG Lys 10	CTC Leu	GAG Glu	CTT Leu	AAG Lys	GAG Glu 15	ATT Ile	48
GCC Ala	AAG Lys	GAT Asp	TAC Tyr 20	GAA Glu	GTC Val	GGT Gly	TTC Phe	GAT Asp 25	TCG Ser	GTT Val	GTG Val	ACT Thr	GTT Val 30	TTG Leu	GCT Ala	96
TAT Tyr	GTT Val 35	TAC Tyr	AGC Ser	AGC Ser	AGA Arg	GTG Val 40	AGA Arg	CCG Pro	CCG Pro	CCT Pro	AAA Lys	GGA Gly 45	GTT Val	TCT Ser	GAA Glu	144
TGC Cys 50	GCA Ala	GAC Asp	GAG Glu	AAT Asn	TGC Cys	TGC Cys 55	CAC His	GTG Val	GCT Ala	TGC Cys	CGG Arg 60	CCG Pro	GCG Ala	GTG Val	GAT Asp	192
TTC Phe 65	ATG Met	TTG Leu	GAG Glu	GTT Val	CTC Leu 70	TAT Tyr	TTG Leu	GCT Ala	TTC Phe	ATC Ile 75	TTC Phe	AAG Lys	ATC Ile	CCT Pro	GAA Glu 80	240
TTA Leu	ATT Ile	ACT Thr	CTC Leu	TAT Tyr 85	CAG Gln	AGG Arg	CAC His	TTA Leu	TTG Leu 90	GAC Asp	GTT Val	GTA Val	GAC Asp	AAA Lys 95	GTT Val	288
GTT Val	ATA Ile	GAG Glu	GAC Asp 100	ACA Thr	TTG Leu	GTT Val	ATA Ile	CTC Leu 105	AAG Lys	CTT Leu	GCT Ala	AAT Asn	ATA Ile 110	TGT Cys	GGT Gly	336
AAA Lys	GCT Ala	TGT Cys 115	ATG Met	AAG Lys	CTA Leu	TTG Leu	GAT Asp 120	AGA Arg	TGT Cys	AAA Lys	GAG Glu	ATT Ile 125	ATT Ile	GTC Val	AAG Lys	384
TCT Ser 130	AAT Asn	GTA Val	GAT Asp	ATG Met	GTT Val	AGT Ser	CTT Leu 135	GAA Glu	AAG Lys	TCA Ser	TTG Leu 140	CCG Pro	GAA Glu	GAG Glu	CTT Leu	432
GTT Val 145	AAA Lys	GAG Glu	ATA Ile	ATT Ile	GAT Asp 150	AGA Arg	CGT Arg	AAA Lys	GAG Glu	CTT Leu 155	GGT Gly	TTG Leu	GAG Glu	GTA Val	CCT Pro 160	480
AAA Lys	GTA Val	AAG Lys	AAA Lys	CAT His 165	GTC Val	TCG Ser	AAT Asn	GTA Val	CAT His 170	AAG Lys	GCA Ala	CTT Leu	GAC Asp	TCG Ser 175	GAT Asp	528
GAT Asp	ATT Ile	GAG Glu	TTA Leu 180	GTC Val	AAG Lys	TTG Leu	CTT Leu	TTG Leu 185	AAA Lys	GAG Glu	GAT Asp	CAC His	ACC Thr 190	AAT Asn	CTA Leu	576
GAT Asp	GAT Asp	GCG Ala 195	TGT Cys	GCT Ala	CTT Leu	CAT His	TTC Phe 200	GCT Ala	GTT Val	GCA Ala	TAT Tyr	TGC Cys 205	AAT Asn	GTG Val	AAG Lys	624
ACC Thr 210	GCA Ala	ACA Thr	GAT Asp	CTT Leu	TTA Leu	AAA Lys 215	CTT Leu	GAT Asp	CTT Leu	GCC Ala	GAT Asp 220	GTC Val	AAC Asn	CAT His	AGG Arg	672
AAT Asn 225	CCG Pro	AGG Arg	GGA Gly	TAT Tyr	ACG Thr	GTG Val 230	CTT Leu	CAT His	GTT Val	GCT Ala 235	GCG Ala	ATG Met	CGG Arg	AAG Lys	GAG Glu 240	720
CCA Pro	CAA Gln	TTG Leu	ATA Ile	CTA Leu 245	TCT Ser	CTA Leu	TTG Leu	GAA Glu	AAA Lys 250	GGT Gly	GCA Ala	AGT Ser	GCA Ala	TCA Ser 255	GAA Glu	768

786

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

Met Asp Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile
1 5 10 15

Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala
20 25 30

Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu
35 40 45

Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp
50 55 60

Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu
65 70 75 80

Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys Val
85 90 95

Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys Gly
100 105 110

Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys
115 120 125

Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu Leu
130 135 140

Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val Pro
145 150 155 160

Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp
165 170 175

Asp Ile Glu Leu Val Lys Leu Leu Lys Glu Asp His Thr Asn Leu
180 185 190

Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val Lys
195 200 205

Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His Arg
210 215 220

Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg Lys Glu
225 230 235 240

Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala Ser Glu
245 250 255

Ala Thr Leu Glu Gly *

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val
1          5          10          15

Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala
          20          25          30

Val His Tyr Ala Val Gln His Cys Asn
          35          40

```

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Pro Thr Gly Lys Thr Ala Leu His Leu Ala Ala Glu Met Val Ser Pro
1          5          10          15

Asp Met Val Ser Val Leu Leu Asp His His Ala Asp Xaa Asn Phe Arg
          20          25          30

Thr Xaa Asp Gly Val Thr
          35

```

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

10016336.121201

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val
1 5 10 15

Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala
20 25 30

Val His Tyr Ala Val Gln His Cys Asn
35 40

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg Arg Pro Asp Ser Lys Thr Ala Leu His Leu Ala Ala Glu Met Val
1 5 10 15

Ser Pro Asp Met Val Ser Val Leu Leu Asp Gln
20 25

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val
1 5 10 15

Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala
20 25 30

Val His Tyr Ala Val Gln His Cys Asn
35 40

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

10016236.12120.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Arg Arg Pro Asp Ser Lys Thr Ala Leu His Leu Ala Ala Glu Met Val
1 5 10 15
Ser Pro Asp Met Val Ser Val Leu Leu Asp Gln
20 25

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ile Arg Arg Met Arg Arg Ala Leu Asp Ala Ala Asp Ile Glu Leu Val
1 5 10 15
Lys Leu Met Val Met Gly Glu Gly Leu Asp Leu Asp Asp Ala Leu Ala
20 25 30
Val His Tyr Ala Val Gln His Cys Asn
35 40

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro Thr Gly Lys Thr Ala Leu His Leu Ala Ala Glu Met Val Ser Pro
1 5 10 15
Asp Met Val

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

10016236 121201

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAACAGCTTC GAAGCCGTCT TTGACGCGCC GGATG

35

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CATCCGGCGC GTCAAAGACG GCTTCGAAGC TGTTG

35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGAATTCAAT GGATTCGGTT GTGACTGTTT TG

32

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGAATTCTAC AAATCTGTAT ACCATTGG

28

(2) INFORMATION FOR SEQ ID NO:29:

10016236.12001

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CGGAATTCGA TCTCTTTAAT TTGTGAATTT C

31

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGAATTCTCA ACAGTTCATA ATCTGGTCG

29

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGAATTCAAT GGACTCCAAC AACACCGCCG C

31

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

10016236 121204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGAATTCTCA ACCTTCCAAA GTTGCTTCTG ATG

33

10016236 121201